



4200.000200

GENERAL INFORMATION:

- (i) APPLICANT: Price, David H.
- (ii) TITLE OF INVENTION: P-TEFb COMPOSITIONS, METHODS AND SCREENING ASSAYS
- (iii) NUMBER OF SEQUENCES: 68
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Williams, Morgan & Amerson, P.C.
 - (B) STREET: 10333 Richmond, #1100
 - (C) CITY: Houston
 - (D) STATE: TX
 - (E) COUNTRY: USA
 - (F) ZIP: 77042
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/951,188
 - (B) FILING DATE: 1997-10-15
 - (C) CLASSIFICATION: Unknown
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Fussey, Shelley P.M.
 - (B) REGISTRATION NUMBER: 39,458
 - (C) REFERENCE/DOCKET NUMBER: 4200.000200
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (713) 934-7000
 - (B) TELEFAX: (713) 934-7011

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1457 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 115..1326
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGTTGAGTCA ACAGCTGTAG ATACACCAAT TGTTGCCGAT TTCTTTCTTT TCGACTGTCTG	60
GCTTCTCGCG AAAGTGTGAT TGTGAAAATT GTACAAATAG AGGCAAATTT AACC ATG	117
	Met
	1
GCG CAC ATG TCC CAC ATG CTC CAG CAG CCT TCG GGG TCG ACG CCC TCC	165
Ala His Met Ser His Met Leu Gln Gln Pro Ser Gly Ser Thr Pro Ser	
5 10 15	

AAC GTG GGC TCC AGC TCA TCG CGC ACG ATG TCC CTG ATG GAG AAA CAA	213
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Asn	Val	Gly	Ser	Ser	Ser	Ser	Arg	Thr	Met	Ser	Leu	Met	Glu	Lys	Gln	
		20					25					30				
AAG	TAC	ATC	GAG	GAC	TAC	GAC	TTT	CCC	TAC	TGC	GAC	GAG	AGC	AAC	AAA	261
Lys	Tyr	Ile	Glu	Asp	Tyr	Asp	Phe	Pro	Tyr	Cys	Asp	Glu	Ser	Asn	Lys	
	35					40					45					
TAC	GAA	AAG	GTG	GCG	AAA	ATT	GGC	CAA	GGC	ACC	TTC	GGA	GAG	GTT	TTT	309
Tyr	Glu	Lys	Val	Ala	Lys	Ile	Gly	Gln	Gly	Thr	Phe	Gly	Glu	Val	Phe	
	50				55					60					65	
AAG	GCT	CGC	GAG	AAA	AAG	GGC	AAC	AAG	AAG	TTT	GTG	GCC	ATG	AAG	AAG	357
Lys	Ala	Arg	Glu	Lys	Lys	Gly	Asn	Lys	Lys	Phe	Val	Ala	Met	Lys	Lys	
				70					75					80		
GTG	CTG	ATG	GAC	AAC	GAA	AAG	GAG	GGC	TTT	CCC	ATC	ACG	GCT	CTG	CGA	405
Val	Leu	Met	Asp	Asn	Glu	Lys	Glu	Gly	Phe	Pro	Ile	Thr	Ala	Leu	Arg	
			85					90					95			
GAG	ATC	CGC	ATC	CTG	CAG	CTG	CTA	AAG	CAC	GAG	AAC	GTG	GTG	AAT	CTG	453
Glu	Ile	Arg	Ile	Leu	Gln	Leu	Leu	Lys	His	Glu	Asn	Val	Val	Asn	Leu	
		100					105					110				
ATC	GAG	ATC	TGC	CGC	ACC	AAG	GCC	ACC	GCC	ACG	AAT	GGT	TAC	AGA	TCC	501
Ile	Glu	Ile	Cys	Arg	Thr	Lys	Ala	Thr	Ala	Thr	Asn	Gly	Tyr	Arg	Ser	
	115					120					125					
ACC	TTC	TAT	TTG	GTC	TTT	GAT	TTC	TGC	GAA	CAC	GAT	TTG	GCA	GGT	CTT	549
Thr	Phe	Tyr	Leu	Val	Phe	Asp	Phe	Cys	Glu	His	Asp	Leu	Ala	Gly	Leu	
	130				135					140					145	
CTG	TCC	AAC	ATG	AAC	GTC	AAG	TTC	AGT	CTG	GGC	GAG	ATT	AAG	AAG	GTT	597
Leu	Ser	Asn	Met	Asn	Val	Lys	Phe	Ser	Leu	Gly	Glu	Ile	Lys	Lys	Val	
				150					155					160		
ATG	CAG	CAG	CTT	TTA	AAC	GGT	TTG	TAT	TAC	ATC	CAC	AGC	AAC	AAG	ATC	645
Met	Gln	Gln	Leu	Leu	Asn	Gly	Leu	Tyr	Tyr	Ile	His	Ser	Asn	Lys	Ile	
			165					170					175			
CTG	CAC	CGA	GAC	ATG	AAA	GCT	GCC	AAC	GTG	CTG	ATT	ACC	AAG	CAT	GGC	693
Leu	His	Arg	Asp	Met	Lys	Ala	Ala	Asn	Val	Leu	Ile	Thr	Lys	His	Gly	
		180					185					190				
ATC	TTA	AAG	CTG	GCT	GAC	TTT	GGC	TTG	GCC	CGT	GCT	TTT	AGC	ATT	CCA	741
Ile	Leu	Lys	Leu	Ala	Asp	Phe	Gly	Leu	Ala	Arg	Ala	Phe	Ser	Ile	Pro	
	195					200					205					
AAG	AAC	GAG	AGT	AAG	AAT	CGC	TAT	ACC	AAT	CGC	GTA	GTA	ACC	TTG	TGG	789
Lys	Asn	Glu	Ser	Lys	Asn	Arg	Tyr	Thr	Asn	Arg	Val	Val	Thr	Leu	Trp	
	210				215					220					225	
TAC	CGG	CCG	CCT	GAG	CTG	CTA	CTT	GGT	GAC	CGC	AAC	TAT	GGT	CCA	CCC	837
Tyr	Arg	Pro	Pro	Glu	Leu	Leu	Leu	Gly	Asp	Arg	Asn	Tyr	Gly	Pro	Pro	
				230					235					240		
GTG	GAC	ATG	TGG	GGA	GCC	GGC	TGC	ATA	ATG	GCC	GAG	ATG	TGG	ACA	CGC	885
Val	Asp	Met	Trp	Gly	Ala	Gly	Cys	Ile	Met	Ala	Glu	Met	Trp	Thr	Arg	
			245					250					255			
TCG	CCC	ATC	ATG	CAA	GGC	AAT	ACG	GAG	CAG	CAG	CAG	TTA	ACC	TTT	ATT	933
Ser	Pro	Ile	Met	Gln	Gly	Asn	Thr	Glu	Gln	Gln	Gln	Leu	Thr	Phe	Ile	
		260					265					270				

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TCG	CAG	CTA	TGC	GGC	TCC	TTT	ACG	CCG	GAC	GTG	TGG	CCG	GGA	GTG	GAG	981
Ser	Gln	Leu	Cys	Gly	Ser	Phe	Thr	Pro	Asp	Val	Trp	Pro	Gly	Val	Glu	
	275					280					285					
GAG	CTG	GAG	CTG	TAC	AAA	TCC	ATC	GAG	CTG	CCA	AAG	AAC	CAG	AAG	CGT	1029
Glu	Leu	Glu	Leu	Tyr	Lys	Ser	Ile	Glu	Leu	Pro	Lys	Asn	Gln	Lys	Arg	
	290				295					300					305	
CGA	GTC	AAG	GAG	CGC	CTG	CGT	CCG	TAT	GTC	AAG	GAT	CAA	ACC	GGC	TGT	1077
Arg	Val	Lys	Glu	Arg	Leu	Arg	Pro	Tyr	Val	Lys	Asp	Gln	Thr	Gly	Cys	
				310					315					320		
GAT	CTA	TTG	GAC	AAA	TTG	CTG	ACC	CTT	GAT	CCC	AAG	AAA	CGC	ATC	GAT	1125
Asp	Leu	Leu	Asp	Lys	Leu	Leu	Thr	Leu	Asp	Pro	Lys	Lys	Arg	Ile	Asp	
			325					330					335			
GCG	GAC	ACA	GCT	CTG	AAT	CAC	GAC	TTC	TTC	TGG	ACG	GAT	CCC	ATG	CCC	1173
Ala	Asp	Thr	Ala	Leu	Asn	His	Asp	Phe	Phe	Trp	Thr	Asp	Pro	Met	Pro	
		340					345					350				
AGC	GAC	TTG	AGC	AAG	ATG	CTG	TCC	CAG	CAC	CTG	CAG	AGC	ATG	TTC	GAG	1221
Ser	Asp	Leu	Ser	Lys	Met	Leu	Ser	Gln	His	Leu	Gln	Ser	Met	Phe	Glu	
	355					360					365					
TAC	CTG	GCG	CAG	CCA	CGC	CGC	AGC	AAC	CAG	ATG	CGC	AAC	TAT	CAC	CAG	1269
Tyr	Leu	Ala	Gln	Pro	Arg	Arg	Ser	Asn	Gln	Met	Arg	Asn	Tyr	His	Gln	
	370				375					380					385	
CAA	CTG	ACC	ACC	ATG	AAC	CAG	AAG	CCC	CAG	GAC	AAC	AGT	ATG	ATT	GAC	1317
Gln	Leu	Thr	Thr	Met	Asn	Gln	Lys	Pro	Gln	Asp	Asn	Ser	Met	Ile	Asp	
				390					395					400		
CGG	GTT	TGG	TAGACTGCCA	GAGGTGTACG	CACCCGACTA	ATAGTTTCTC										1366
Arg	Val	Trp														
ACCTTCAACT	AGCGTTAGGT	TATTAGGTTA	GTGTACAATA	AAAATATTGG	CATTTGCATT											1426
AGCGCTTGCT	CCAAATATAA	AAAAAAAAAA	A													1457

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ala	His	Met	Ser	His	Met	Leu	Gln	Gln	Pro	Ser	Gly	Ser	Thr	Pro	
1				5					10					15		
Ser	Asn	Val	Gly	Ser	Ser	Ser	Ser	Arg	Thr	Met	Ser	Leu	Met	Glu	Lys	
		20						25				30				
Gln	Lys	Tyr	Ile	Glu	Asp	Tyr	Asp	Phe	Pro	Tyr	Cys	Asp	Glu	Ser	Asn	
		35				40					45					
Lys	Tyr	Glu	Lys	Val	Ala	Lys	Ile	Gly	Gln	Gly	Thr	Phe	Gly	Glu	Val	
	50					55					60					

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Phe Lys Ala Arg Glu Lys Lys Gly Asn Lys Lys Phe Val Ala Met Lys
 65 70 75 80
 Lys Val Leu Met Asp Asn Glu Lys Glu Gly Phe Pro Ile Thr Ala Leu
 85 90 95
 Arg Glu Ile Arg Ile Leu Gln Leu Leu Lys His Glu Asn Val Val Asn
 100 105 110
 Leu Ile Glu Ile Cys Arg Thr Lys Ala Thr Ala Thr Asn Gly Tyr Arg
 115 120 125
 Ser Thr Phe Tyr Leu Val Phe Asp Phe Cys Glu His Asp Leu Ala Gly
 130 135 140
 Leu Leu Ser Asn Met Asn Val Lys Phe Ser Leu Gly Glu Ile Lys Lys
 145 150 155 160
 Val Met Gln Gln Leu Leu Asn Gly Leu Tyr Tyr Ile His Ser Asn Lys
 165 170 175
 Ile Leu His Arg Asp Met Lys Ala Ala Asn Val Leu Ile Thr Lys His
 180 185 190
 Gly Ile Leu Lys Leu Ala Asp Phe Gly Leu Ala Arg Ala Phe Ser Ile
 195 200 205
 Pro Lys Asn Glu Ser Lys Asn Arg Tyr Thr Asn Arg Val Val Thr Leu
 210 215 220
 Trp Tyr Arg Pro Pro Glu Leu Leu Leu Gly Asp Arg Asn Tyr Gly Pro
 225 230 235 240
 Pro Val Asp Met Trp Gly Ala Gly Cys Ile Met Ala Glu Met Trp Thr
 245 250 255
 Arg Ser Pro Ile Met Gln Gly Asn Thr Glu Gln Gln Gln Leu Thr Phe
 260 265 270
 Ile Ser Gln Leu Cys Gly Ser Phe Thr Pro Asp Val Trp Pro Gly Val
 275 280 285
 Glu Glu Leu Glu Leu Tyr Lys Ser Ile Glu Leu Pro Lys Asn Gln Lys
 290 295 300
 Arg Arg Val Lys Glu Arg Leu Arg Pro Tyr Val Lys Asp Gln Thr Gly
 305 310 315 320
 Cys Asp Leu Leu Asp Lys Leu Leu Thr Leu Asp Pro Lys Lys Arg Ile
 325 330 335
 Asp Ala Asp Thr Ala Leu Asn His Asp Phe Phe Trp Thr Asp Pro Met
 340 345 350
 Pro Ser Asp Leu Ser Lys Met Leu Ser Gln His Leu Gln Ser Met Phe
 355 360 365
 Glu Tyr Leu Ala Gln Pro Arg Arg Ser Asn Gln Met Arg Asn Tyr His
 370 375 380
 Gln Gln Leu Thr Thr Met Asn Gln Lys Pro Gln Asp Asn Ser Met Ile
 385 390 395 400

Asp Arg Val Trp

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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CAGCCCTGCC GACGGCCATA CTTGAAAATA CATTTTTTTC TGCAAAGTTT GTCATTGTCA    60
CTGTGTGAAT GGAATCTGTG ATGTGTTGTG GAATTAAAAA CGTCAAGTAA ACAACCCGTA    120
ATGGTTAAAG TGCACGGCGA AAGCAGTGCG AATAACTATG AATTGATACA AAAGTTGCAT    180
AACACGTCGC CTGGTGTCTG GGTAGTGTG TTTTTCGTCT CGTTTCGTTT CCGCCGCGT    240
CGCAGTTTCC AAAAAACCTC ACCACACCAT ACCATCTCCA CCACGCACAC ACACACACAA    300
ACAAACACGC AGAGACGCGG CGGCGGAAAA AGTGTGCGGA CCGCGGATTT AACCCCTCGT    360
TCCAAACCCA AATTGGAGTC TCCCAAAAAC AGCGAAATAT CGAGTGTGGC TTAGCCGATG    420
TGCCGTGCGA TCCCCACTGC CCCTTCCGTA CCGCTGCCAC CCCC GCCACA GCAGCAACGC    480
ACACGGATAC GGACACAGAC ACCAATACCA GCGCACTCAA GCACGGCCGA CAAAGAAAGA    540
GCGCTCTCCC TTCCTCTTTG TACAGTTAGT TCCTACAGCT GAATCAGCCA AAAGAAATTA    600
CTAGGTCCAT TCCGAGGCGC AGTTTGCATG TGAAACGGAG GTCCCCGCAT AACCACGCGG    660
AACCCGAAAT TCCAGATCCC CATCTCCGCT GCACGGATAA AGGAAACATA CAACCATGAG    720
TCTCCTAGCC ACGCCAATGC CCCAGGCGGC CACCGCCTCA TCTTCTTCAT CCGCCTCCGC    780
GGCCGCTCTG GCCAGCGGGA TTCCAATCAC CGCCAACAAC AACCTGCCTT TCGAGAAGGA    840
CAAGATCTGG TACTTCAGCA ACGATCAGCT GGCCAATTTG CCAAGCAGAA GATGCGGCAT    900
CAAGGGCGAC GATGAGCTGC AGTACCGCCA GATGACCGCC TATCTGATAC AGGAAATGGG    960
TCAGCGTCTG CAGGTGTCCC AACTGTGCAT CAACACGGCC ATTGTGTACA TGCATCGGTT   1020
CTACGCCTTT CACTCCTTCA CCCACTTTCA TCGCAACTCC ATGGCGTCGG CGAGCCTCTT   1080
CTTGGCCGCC AAGGTAGAAG AGCAACCGCG GAAGCTGGAG CATGTTATTC GGGCCGCCAA   1140
CAAGTGCCTG CCGCCGACCA CCGAGCAGAA TTACGCCGAA CTCGCCCAGG AGCTTGTGTT   1200
CAACGAGAAC GTGCTCCTGC AGACGCTGGG CTTCGATGTG GCCATCGATC ATCCGCACAC   1260
GCATGTGGTG CGCACCTGCC AGCTGGTCAA AGCATGCAAG GATCTGGCGC AGACATCGTA   1320
CTTCTTGGCC TCGAACAGCC TGCATCTGAC CTCGATGTGC CTCCAATATC GCCCCACGGT   1380
CGTAGCCTGT TTCTGCATTT ACCTAGCCTG CAAGTGGTCC CGATGGGAGA TCCCCCAGTC   1440

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GACCGAGGGC	AAGCACTGGT	TCTACTATGT	GGACAAGACG	GTCTCGCTGG	ATTTGCTAAA	1500
GCAGCTGACA	GATGAGTTCA	TCGCTATCTA	TGAGAAGAGC	CCGGCCCCGTC	TGAAGTCTAA	1560
GCTTAACTCG	ATCAAGGCGA	TCGCCCAGGG	AGCCAGCAAT	CGGACAGCTA	ACAGCAAGGA	1620
CAAACCAAAG	GAGGACTGGA	AGATCACCGA	GATGATGAAG	GGCTACCACT	CAAACATCAC	1680
GACACCACCA	GAGCTGTAA	ACGGCAACGA	CAGCCGGGAT	CGGGACCGAG	ATCGTGAACG	1740
GGAGAGAGAG	CGGGAACGGG	ATCCGTCTGC	ACTACTGCCG	CCACCGGCTA	TGGTGCCGCA	1800
GCAAAGACGA	CAGGATGGTG	GACATCAGCG	CTCGTCCTCA	GTGAGCGGAG	TGCCAGGCAG	1860
CAGCTCTTCG	TCGTCTTCCT	CCAGTCACAA	GATGCCAAAT	TACCCTGGTG	GCATGCCGCC	1920
CGAAGCTCAT	CCGGATCACA	AGTCAAAGCA	GCCGGGCTAT	AACAATCGAA	TGCCCTCAAG	1980
TCACCAGCGT	AGTAGTAGCA	GTGGACTCGG	TTCCTCGGGA	AGTGGCAGCC	AGCACAGCAG	2040
CTCATCCTCG	TCGTCTTCAA	GCCAGCAGCC	TGGCCGACCG	TCTATGCCCG	TGGACTATCA	2100
CAAATCCTCT	CGCGGCATGC	CGCCGGTAGG	CGTGGGCATG	CCACCTCACG	GCAGCCACAA	2160
GATGACTTCG	GGCTCCAAGC	CTCAACAGCC	GCAGCAGCAG	CCGGTCCCAC	ATCCATCCGC	2220
CTCTAATTCC	TCTGCATCGG	GCATGTCCTC	CAAGGATAAA	TCCCAGAGCA	ACAAAATGTA	2280
TCCGAACGCA	CCGCCGCCAT	ACAGTAATAG	TGCCCCCTAA	AACCCGCTGA	TGTCGCGTGG	2340
TGGATATCCA	GGCGCTAGCA	ATGGATCCCA	GCCCCCGCCT	CCCGCCGGAT	ACGGCGGCCA	2400
TCGCAGCAAA	TCCGGCTCCA	CCGTCCATGG	CATGCCGCAT	TTCGAGCAGC	AATTGCCCTA	2460
TTCCCAGAGC	CAGAGCTACG	GCCACATGCA	GCAGCAGCCA	GTGCCTCAGT	CTCAGCAGCA	2520
ACAGATGCCT	CCGGAGGCAT	CCCAGCACTC	GTTGCAGTCC	AAGAACTCGC	TCTTCAGTCC	2580
AGAGTGGCCA	GACATTAATA	AGGAGCCCAT	GTCGCAGTCG	CAACCACAGC	TTTTTAACGG	2640
TTTGCTACCC	CCTCCTGCGC	CTCCCGGCCA	CGATTACAAG	CTAAATAGCC	ATCCGCGCGA	2700
CAAAGAAAGT	CCCAAGAAAG	AGCGACTAAC	GCCAACCAAA	AAGGATAAGC	ACCGTCCTGT	2760
AATGCCCCCA	ATGGGCAGTG	GGAACAGTTC	CTCCGGCTCG	GGATCATCAA	AGCCGATGCT	2820
ACCGCCTCAC	AAGAAGCAGA	TACCCCATGG	CGGGGACCTG	TTGACCAATC	CTGGAGAGAG	2880
TGGAAGCCTA	AAACGGCCCA	ACGAGATCTC	GGGAAGTCAG	TATGGACTAA	ATAAGCTGGA	2940
TGAAATAGAT	AACAGTAATA	TGCCTCGAGA	AAAGCTTCGC	AAGCTGGACA	CTACAACTGG	3000
ACTACCAACT	TATCCGAATT	ATGAGGAGAA	ACACACGCCT	CTGAATATGT	CCAACGGAAT	3060
CGAGACAACG	CCGGATCTGG	TGCGCAGTTT	GCTAAAGGAG	AGTCTGTGTC	CATCGAACGC	3120
TTCGCTCCTG	AAACCGGATG	CCTTGACTAT	GCCTGGCCTG	AAACCACCGG	CCGAACACT	3180
TGAGCCCATG	CCCGCACCAG	CGACAATCAA	GAAAGAACAG	GGAATAACTC	CGATGACCAG	3240
TTTGGCTAGT	GGGCCCCGAC	CCATGGATTT	GGAAGTACCC	ACTAAACAGG	CCGGAGAGAT	3300
TAAGGAGGAA	AGCAGCAGCA	AGTCCGAAAA	GAAAAAGAAG	AAGGATAAAC	ACAAACACAA	3360

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GGAGAAGGAC AAGTCCAAGG ACAAGACGGA AAAGGAGGAG CGTAAGAAGC ACAAGAGGGA 3420
CAAGCAGAAG GATCGTAGCG GCAGCGGTGG CAGCAAGGAC AGTTCTCTTC CCAATGAGCC 3480
TCTGAAGATG GTTATCAAGA ATCCCAACGG CAGCCTGCAG GCCGGTGCGT CAGCTCCCAT 3540
TAAACTTAAG ATCAGCAAAA ATAAGGTTGA ACCCAATAAC TACTCTGCAG CGGCGGGTCT 3600
GCCTGGCGCA ATCGGATATG GCTTGCCTCC AACTACGGCT ACCACCACAT CCGCTTCGAT 3660
CGGAGCAGCT GCTCCTGTTC TGCCTCCTTA TGGTGCCGGC GGTGGTGGCT ACAGCTCATC 3720
GGGCGGCAGC AGTTCCGGTG GCAGCAGCAA GAAAAAGCAC AGCGATCGTG ACCGCGACAA 3780
GGAGAGCAAA AAGAATAAGA GCCAAGACTA CGCGAAGTAC AATGGCGCTG GTGGCGGCAT 3840
CTTTAATCCC CTTGGCGGTG CTGGCGCCGC ACCCAATATG TCTGGAGGAA TGGGCGCCCC 3900
CATGTCTACT GCTGTACCAC CATCCATGCT GTTGGCGCCC ACCGGTGCAG TACCACCCTC 3960
TGCCGCTGGG CTGGCACCGC CTCCCATGCC CGTCTACAAC AAGAAGTAGT GGTAGCGGTC 4020
AGAGGGTTAT TCTTAAGTCG TACGTTTTGA TATATGTATA GAACCTCAGT AAGTCCGATT 4080
GTAGTATAGT TGTTAGGATT GTTAGTGAGA TGCATTATTG ATTTTAGTTA AGCACATAGA 4140
TAAAACTCCA AATTGGAAGT GAAACCGGAT GCGCAGATCG AAGAAGAATG GAAGTAGATG 4200
TCGCGATGGG GCTGGACGTA AAAGCAGTAC TCAAATCGCG AAAACTTTTG TACAGCATT 4260
ATTAGTTTAT AACTATAATA AATAGCATAC ATATAAGCCC AAAAAAAAAA AAAAAAAAAA 4320
AAAAAAAAA 4328

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1097 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Met Ser Leu Leu Ala Thr Pro Met Pro Gln Ala Ala Thr Ala Ser Ser
1          5          10          15
Ser Ser Ser Ala Ser Ala Ala Ala Ser Ala Ser Gly Ile Pro Ile Thr
20          25          30
Ala Asn Asn Asn Leu Pro Phe Glu Lys Asp Lys Ile Trp Tyr Phe Ser
35          40          45
Asn Asp Gln Leu Ala Asn Leu Pro Ser Arg Arg Cys Gly Ile Lys Gly
50          55          60
Asp Asp Glu Leu Gln Tyr Arg Gln Met Thr Ala Tyr Leu Ile Gln Glu
65          70          75          80
Met Gly Gln Arg Leu Gln Val Ser Gln Leu Cys Ile Asn Thr Ala Ile
85          90          95

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Val	Tyr	Met	His	Arg	Phe	Tyr	Ala	Phe	His	Ser	Phe	Thr	His	Phe	His
			100					105					110		
Arg	Asn	Ser	Met	Ala	Ser	Ala	Ser	Leu	Phe	Leu	Ala	Ala	Lys	Val	Glu
		115					120					125			
Glu	Gln	Pro	Arg	Lys	Leu	Glu	His	Val	Ile	Arg	Ala	Ala	Asn	Lys	Cys
	130					135					140				
Leu	Pro	Pro	Thr	Thr	Glu	Gln	Asn	Tyr	Ala	Glu	Leu	Ala	Gln	Glu	Leu
145					150					155					160
Val	Phe	Asn	Glu	Asn	Val	Leu	Leu	Gln	Thr	Leu	Gly	Phe	Asp	Val	Ala
				165					170					175	
Ile	Asp	His	Pro	His	Thr	His	Val	Val	Arg	Thr	Cys	Gln	Leu	Val	Lys
			180					185					190		
Ala	Cys	Lys	Asp	Leu	Ala	Gln	Thr	Ser	Tyr	Phe	Leu	Ala	Ser	Asn	Ser
		195					200					205			
Leu	His	Leu	Thr	Ser	Met	Cys	Leu	Gln	Tyr	Arg	Pro	Thr	Val	Val	Ala
	210					215					220				
Cys	Phe	Cys	Ile	Tyr	Leu	Ala	Cys	Lys	Trp	Ser	Arg	Trp	Glu	Ile	Pro
225					230					235					240
Gln	Ser	Thr	Glu	Gly	Lys	His	Trp	Phe	Tyr	Tyr	Val	Asp	Lys	Thr	Val
				245					250					255	
Ser	Leu	Asp	Leu	Leu	Lys	Gln	Leu	Thr	Asp	Glu	Phe	Ile	Ala	Ile	Tyr
			260					265					270		
Glu	Lys	Ser	Pro	Ala	Arg	Leu	Lys	Ser	Lys	Leu	Asn	Ser	Ile	Lys	Ala
		275					280					285			
Ile	Ala	Gln	Gly	Ala	Ser	Asn	Arg	Thr	Ala	Asn	Ser	Lys	Asp	Lys	Pro
	290					295					300				
Lys	Glu	Asp	Trp	Lys	Ile	Thr	Glu	Met	Met	Lys	Gly	Tyr	His	Ser	Asn
305					310					315					320
Ile	Thr	Thr	Pro	Pro	Glu	Leu	Leu	Asn	Gly	Asn	Asp	Ser	Arg	Asp	Arg
				325					330					335	
Asp	Arg	Asp	Arg	Glu	Arg	Glu	Arg	Glu	Arg	Glu	Arg	Asp	Pro	Ser	Ser
			340					345					350		
Leu	Leu	Pro	Pro	Pro	Ala	Met	Val	Pro	Gln	Gln	Arg	Arg	Gln	Asp	Gly
		355					360					365			
Gly	His	Gln	Arg	Ser	Ser	Ser	Val	Ser	Gly	Val	Pro	Gly	Ser	Ser	Ser
	370					375					380				
Ser	Ser	Ser	Ser	Ser	Ser	His	Lys	Met	Pro	Asn	Tyr	Pro	Gly	Gly	Met
385					390					395					400
Pro	Pro	Glu	Ala	His	Pro	Asp	His	Lys	Ser	Lys	Gln	Pro	Gly	Tyr	Asn
				405					410					415	
Asn	Arg	Met	Pro	Ser	Ser	His	Gln	Arg	Ser	Ser	Ser	Ser	Gly	Leu	Gly
			420					425					430		

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Ser Ser Gly Ser Gly Ser Gln His Ser Ser Ser Ser Ser Ser Ser Ser
435 440 445
Ser Gln Gln Pro Gly Arg Pro Ser Met Pro Val Asp Tyr His Lys Ser
450 455 460
Ser Arg Gly Met Pro Pro Val Gly Val Gly Met Pro Pro His Gly Ser
465 470 475 480
His Lys Met Thr Ser Gly Ser Lys Pro Gln Gln Pro Gln Gln Gln Pro
485 490 495
Val Pro His Pro Ser Ala Ser Asn Ser Ser Ala Ser Gly Met Ser Ser
500 505 510
Lys Asp Lys Ser Gln Ser Asn Lys Met Tyr Pro Asn Ala Pro Pro Pro
515 520 525
Tyr Ser Asn Ser Ala Pro Gln Asn Pro Leu Met Ser Arg Gly Gly Tyr
530 535 540
Pro Gly Ala Ser Asn Gly Ser Gln Pro Pro Pro Ala Gly Tyr Gly
545 550 555 560
Gly His Arg Ser Lys Ser Gly Ser Thr Val His Gly Met Pro His Phe
565 570 575
Glu Gln Gln Leu Pro Tyr Ser Gln Ser Gln Ser Tyr Gly His Met Gln
580 585 590
Gln Gln Pro Val Pro Gln Ser Gln Gln Gln Gln Met Pro Pro Glu Ala
595 600 605
Ser Gln His Ser Leu Gln Ser Lys Asn Ser Leu Phe Ser Pro Glu Trp
610 615 620
Pro Asp Ile Lys Lys Glu Pro Met Ser Gln Ser Gln Pro Gln Leu Phe
625 630 635 640
Asn Gly Leu Leu Pro Pro Pro Ala Pro Pro Gly His Asp Tyr Lys Leu
645 650 655
Asn Ser His Pro Arg Asp Lys Glu Ser Pro Lys Lys Glu Arg Leu Thr
660 665 670
Pro Thr Lys Lys Asp Lys His Arg Pro Val Met Pro Pro Met Gly Ser
675 680 685
Gly Asn Ser Ser Ser Gly Ser Gly Ser Ser Lys Pro Met Leu Pro Pro
690 695 700
His Lys Lys Gln Ile Pro His Gly Gly Asp Leu Leu Thr Asn Pro Gly
705 710 715 720
Glu Ser Gly Ser Leu Lys Arg Pro Asn Glu Ile Ser Gly Ser Gln Tyr
725 730 735
Gly Leu Asn Lys Leu Asp Glu Ile Asp Asn Ser Asn Met Pro Arg Glu
740 745 750
Lys Leu Arg Lys Leu Asp Thr Thr Thr Gly Leu Pro Thr Tyr Pro Asn
755 760 765

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Tyr Glu Glu Lys His Thr Pro Leu Asn Met Ser Asn Gly Ile Glu Thr
 770 775 780
 Thr Pro Asp Leu Val Arg Ser Leu Leu Lys Glu Ser Leu Cys Pro Ser
 785 790 795 800
 Asn Ala Ser Leu Leu Lys Pro Asp Ala Leu Thr Met Pro Gly Leu Lys
 805 810 815
 Pro Pro Ala Glu Leu Leu Glu Pro Met Pro Ala Pro Ala Thr Ile Lys
 820 825 830
 Lys Glu Gln Gly Ile Thr Pro Met Thr Ser Leu Ala Ser Gly Pro Ala
 835 840 845
 Pro Met Asp Leu Glu Val Pro Thr Lys Gln Ala Gly Glu Ile Lys Glu
 850 855 860
 Glu Ser Ser Ser Lys Ser Glu Lys Lys Lys Lys Lys Asp Lys His Lys
 865 870 875 880
 His Lys Glu Lys Asp Lys Ser Lys Asp Lys Thr Glu Lys Glu Glu Arg
 885 890 895
 Lys Lys His Lys Arg Asp Lys Gln Lys Asp Arg Ser Gly Ser Gly Gly
 900 905 910
 Ser Lys Asp Ser Ser Leu Pro Asn Glu Pro Leu Lys Met Val Ile Lys
 915 920 925
 Asn Pro Asn Gly Ser Leu Gln Ala Gly Ala Ser Ala Pro Ile Lys Leu
 930 935 940
 Lys Ile Ser Lys Asn Lys Val Glu Pro Asn Asn Tyr Ser Ala Ala Ala
 945 950 955 960
 Gly Leu Pro Gly Ala Ile Gly Tyr Gly Leu Pro Pro Thr Thr Ala Thr
 965 970 975
 Thr Thr Ser Ala Ser Ile Gly Ala Ala Ala Pro Val Leu Pro Pro Tyr
 980 985 990
 Gly Ala Gly Gly Gly Gly Tyr Ser Ser Ser Gly Gly Ser Ser Ser Gly
 995 1000 1005
 Gly Ser Ser Lys Lys Lys His Ser Asp Arg Asp Arg Asp Lys Glu Ser
 1010 1015 1020
 Lys Lys Asn Lys Ser Gln Asp Tyr Ala Lys Tyr Asn Gly Ala Gly Gly
 1025 1030 1035 1040
 Gly Ile Phe Asn Pro Leu Gly Gly Ala Gly Ala Ala Pro Asn Met Ser
 1045 1050 1055
 Gly Gly Met Gly Ala Pro Met Ser Thr Ala Val Pro Pro Ser Met Leu
 1060 1065 1070
 Leu Ala Pro Thr Gly Ala Val Pro Pro Ser Ala Ala Gly Leu Ala Pro
 1075 1080 1085
 Pro Pro Met Pro Val Tyr Asn Lys Lys
 1090 1095

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1119 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..1116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG GCA AAG CAG TAC GAC TCG GTG GAG TGC CCT TTT TGT GAT GAA GTT	48
Met Ala Lys Gln Tyr Asp Ser Val Glu Cys Pro Phe Cys Asp Glu Val	
1 5 10 15	
TCC AAA TAC GAG AAG CTC GCC AAG ATC GGC CAA GGC ACC TTC GGG GAG	96
Ser Lys Tyr Glu Lys Leu Ala Lys Ile Gly Gln Gly Thr Phe Gly Glu	
20 25 30	
GTG TTC AAG GCC AGG CAC CGC AAG ACC GGC CAG AAG GTG GCT CTG AAG	144
Val Phe Lys Ala Arg His Arg Lys Thr Gly Gln Lys Val Ala Leu Lys	
35 40 45	
AAG GTG CTG ATG GAA AAC GAG AAG GAG GGG TTC CCC ATT ACA GCC TTG	192
Lys Val Leu Met Glu Asn Glu Lys Glu Gly Phe Pro Ile Thr Ala Leu	
50 55 60	
CGG GAG ATC AAG ATC CTT CAG CTT CTA AAA CAC GAG AAT GTG GTC AAC	240
Arg Glu Ile Lys Ile Leu Gln Leu Leu Lys His Glu Asn Val Val Asn	
65 70 75 80	
TTG ATT GAG ATT TGT CGA ACC AAA GCT TCC CCC TAT AAC CGC TGC AAG	288
Leu Ile Glu Ile Cys Arg Thr Lys Ala Ser Pro Tyr Asn Arg Cys Lys	
85 90 95	
GGT AGT ATA TAC CTG GTG TTC GAC TTC TGC GAG CAT GAC CTT GCT GGG	336
Gly Ser Ile Tyr Leu Val Phe Asp Phe Cys Glu His Asp Leu Ala Gly	
100 105 110	
CTG TTG AGC AAT GTT TTG GTC AAG TTC ACG CTG TCT GAG ATC AAG AGG	384
Leu Leu Ser Asn Val Leu Val Lys Phe Thr Leu Ser Glu Ile Lys Arg	
115 120 125	
GTG ATG CAG ATG CTG CTT AAC GGC CTC TAC TAC ATC CAC AGA AAC AAG	432
Val Met Gln Met Leu Leu Asn Gly Leu Tyr Tyr Ile His Arg Asn Lys	
130 135 140	
ATC CTG CAT AGG GAC ATG AAG GCT GCT AAT GTG CTT ATC ACT CGT GAT	480
Ile Leu His Arg Asp Met Lys Ala Ala Asn Val Leu Ile Thr Arg Asp	
145 150 155 160	
GGG GTC CTG AAG CTG GCA GAC TTT GGG CTG GCC CGG GCC TTC AGC CTG	528
Gly Val Leu Lys Leu Ala Asp Phe Gly Leu Ala Arg Ala Phe Ser Leu	
165 170 175	
GCC AAG AAC AGC CAG CCC AAC CGC TAC ACC AAC CGT GTG GTG ACA CTC	576
Ala Lys Asn Ser Gln Pro Asn Arg Tyr Thr Asn Arg Val Val Thr Leu	
180 185 190	

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TGG Trp	TAC Tyr	CGG Arg	CCC Pro	CCG Pro	GAG Glu	CTG Leu	TTG Leu	CTC Leu	GGG Gly	GAG Glu	CGG Arg	GAC Asp	TAC Tyr	GGC Gly	CCC Pro	624
		195				200						205				
CCC Pro	ATT Ile	GAC Asp	CTG Leu	TGG Trp	GGT Gly	GCT Ala	GGG Gly	TGC Cys	ATC Ile	ATG Met	GCA Ala	GAG Glu	ATG Met	TGG Trp	ACC Thr	672
	210					215					220					
CGC Arg	AGC Ser	CCC Pro	ATC Ile	ATG Met	CAG Gln	GGC Gly	AAC Asn	ACG Thr	GAG Glu	CAG Gln	CAC His	CAA Gln	CTC Leu	GCC Ala	CTC Leu	720
	225				230					235					240	
ATC Ile	AGT Ser	CAG Gln	CTC Leu	TGC Cys	GGC Gly	TCC Ser	ATC Ile	ACC Thr	CCT Pro	GAG Glu	GTG Val	TGG Trp	CCA Pro	AAC Asn	GTG Val	768
			245						250					255		
GAC Asp	AAC Asn	TAT Tyr	GAG Glu	CTG Leu	TAC Tyr	GAA Glu	AAG Lys	CTG Leu	GAG Glu	CTG Leu	GTC Val	AAG Lys	GGC Gly	CAG Gln	AAG Lys	816
			260					265					270			
CGG Arg	AAG Lys	GTG Val	AAG Lys	GAC Asp	AGG Arg	CTG Leu	AAG Lys	GCC Ala	TAT Tyr	GTG Val	CGT Arg	GAC Asp	CCA Pro	TAC Tyr	GCA Ala	864
		275					280					285				
CTG Leu	GAC Asp	CTC Leu	ATC Ile	GAC Asp	AAG Lys	CTG Leu	CTG Leu	GTG Val	CTG Leu	GAC Asp	CCT Pro	GCC Ala	CAG Gln	CGC Arg	ATC Ile	912
	290					295					300					
GAC Asp	AGC Ser	GAT Asp	GAC Asp	GCC Ala	CTC Leu	AAC Asn	CAC His	GAC Asp	TTC Phe	TTC Phe	TGG Trp	TCC Ser	GAC Asp	CCC Pro	ATG Met	960
	305				310					315					320	
CCC Pro	TCC Ser	GAC Asp	CTC Leu	AAG Lys	GGC Gly	ATG Met	CTC Leu	TCC Ser	ACC Thr	CAC His	CTG Leu	ACG Thr	TCC Ser	ATG Met	TTC Phe	1008
				325					330					335		
GAG Glu	TAC Tyr	TTG Leu	GCA Ala	CCA Pro	CCG Pro	CGC Arg	CGG Arg	AAG Lys	GGC Gly	AGC Ser	CAG Gln	ATC Ile	ACC Thr	CAG Gln	CAG Gln	1056
			340					345					350			
TCC Ser	ACC Thr	AAC Asn	CAG Gln	AGT Ser	CGC Arg	AAT Asn	CCC Pro	GCC Ala	ACC Thr	ACC Thr	AAC Asn	CAG Gln	ACG Thr	GAG Glu	TTT Phe	1104
		355					360					365				
GAG Glu	CGC Arg	GTC Val	TTC Phe	TGA												1119
		370														

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Ala	Lys	Gln	Tyr	Asp	Ser	Val	Glu	Cys	Pro	Phe	Cys	Asp	Glu	Val
1				5					10					15	

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Ser Lys Tyr Glu₂₀ Lys Leu Ala Lys Ile₂₅ Gly Gln Gly Thr Phe₃₀ Gly Glu
Val Phe Lys₃₅ Ala Arg His Arg Lys₄₀ Thr Gly Gln Lys Val₄₅ Ala Leu Lys
Lys Val₅₀ Leu Met Glu Asn Glu₅₅ Lys Glu Gly Phe Pro₆₀ Ile Thr Ala Leu
Arg Glu Ile Lys Ile₇₀ Gln Leu Leu Lys His₇₅ Glu Asn Val Val₈₀ Asn
Leu Ile Glu Ile Cys₈₅ Arg Thr Lys Ala Ser₉₀ Pro Tyr Asn Arg Cys₉₅ Lys
Gly Ser Ile Tyr₁₀₀ Leu Val Phe Asp Phe₁₀₅ Cys Glu His Asp Leu₁₁₀ Ala Gly
Leu Leu Ser₁₁₅ Asn Val Leu Val Lys₁₂₀ Phe Thr Leu Ser Glu₁₂₅ Ile Lys Arg
Val Met₁₃₀ Gln Met Leu Leu Asn₁₃₅ Gly Leu Tyr Tyr Ile₁₄₀ His Arg Asn Lys
Ile₁₄₅ Leu His Arg Asp Met₁₅₀ Lys Ala Ala Asn Val₁₅₅ Leu Ile Thr Arg Asp₁₆₀
Gly Val Leu Lys₁₆₅ Leu Ala Asp Phe Gly₁₇₀ Leu Ala Arg Ala Phe Ser₁₇₅ Leu
Ala Lys Asn Ser₁₈₀ Gln Pro Asn Arg Tyr₁₈₅ Thr Asn Arg Val Val₁₉₀ Thr Leu
Trp Tyr Arg₁₉₅ Pro Pro Glu Leu Leu₂₀₀ Leu Gly Glu Arg Asp₂₀₅ Tyr Gly Pro
Pro Ile₂₁₀ Asp Leu Trp Gly Ala₂₁₅ Gly Cys Ile Met Ala₂₂₀ Glu Met Trp Thr
Arg₂₂₅ Ser Pro Ile Met Gln₂₃₀ Gly Asn Thr Glu Gln₂₃₅ His Gln Leu Ala Leu₂₄₀
Ile Ser Gln Leu Cys₂₄₅ Gly Ser Ile Thr Pro₂₅₀ Glu Val Trp Pro Asn Val₂₅₅
Asp Asn Tyr Glu₂₆₀ Leu Tyr Glu Lys₂₆₅ Leu Glu Leu Val Lys₂₇₀ Gly Gln Lys
Arg Lys Val₂₇₅ Lys Asp Arg Leu Lys₂₈₀ Ala Tyr Val Arg Asp₂₈₅ Pro Tyr Ala
Leu Asp₂₉₀ Leu Ile Asp Lys Leu₂₉₅ Leu Val Leu Asp Pro₃₀₀ Ala Gln Arg Ile
Asp₃₀₅ Ser Asp Asp Ala Leu₃₁₀ Asn His Asp Phe Phe₃₁₅ Trp Ser Asp Pro Met₃₂₀
Pro Ser Asp Leu Lys₃₂₅ Gly Met Leu Ser Thr₃₃₀ His Leu Thr Ser Met₃₃₅ Phe
Glu Tyr Leu Ala₃₄₀ Pro Pro Arg Arg Lys₃₄₅ Gly Ser Gln Ile Thr₃₅₀ Gln Gln

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Ser Thr Asn Gln Ser Arg Asn Pro Ala Thr Thr Asn Gln Thr Glu Phe
355 360 365

Glu Arg Val Phe
370

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ACGAATTCCA CACAATCCAA AGATC

25

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CAGAATTCCT ATTGCCGATC CCCAGA

26

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: modified_base
(B) LOCATION: one-of(8, 14)
(D) OTHER INFORMATION: /mod_base= OTHER

/note= "N = A or C or G or T"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
(B) LOCATION: 12
(D) OTHER INFORMATION: /mod_base= OTHER

/note= "Y = C or T"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
(B) LOCATION: one-of(17, 20)
(D) OTHER INFORMATION: /mod_base= OTHER

/note= "R = A or G"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGAATTCNAT GYTNCARCAR CC

22

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: modified_base
 - (B) LOCATION: one-of(13, 16, 19, 22, 25)
 - (D) OTHER INFORMATION: /mod_base= OTHER
- /note= "R = A or G"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AACTGCAGTC CARAARAART CRTGRTT

27

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGTC AAGGAT CAAACCGGCT GTGAT

25

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGAATTCCAA GAAACGCATC GATGC

25

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGACCTGCCA AATCGTGT

18

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

4200.000200

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGAAGGTGGA TCTGTAACCA TTCGT

25

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGAATTCAGA TCTCGATCAG ATTCA

25

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTACTACTCG AGCTACCAAA CCCGGTC

27

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TAAGCAAGCT TCTATGGCGC ACATGTCC

28

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTACTACTCG AGCTACCAAA CCCGGTC

27

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: one-of(13, 16, 22)
- (D) OTHER INFORMATION: /mod_base= OTHER

/note= "Y = C or T"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 17
- (D) OTHER INFORMATION: /mod_base= OTHER

/note= "W = A or T"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /mod_base= OTHER

/note= "S = C or G"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 19
- (D) OTHER INFORMATION: /mod_base= OTHER

/note= "N = A or C or G or T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGAATTCTGG TAYTTYWSNA AYGA

24

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /mod_base= OTHER

/note= "Y = C or T"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 14
- (D) OTHER INFORMATION: /mod_base= OTHER

/note= "R = A or G"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: one-of(17, 20)
- (D) OTHER INFORMATION: /mod_base= OTHER

/note= "N = A or C or G or T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CGGGATCCTG YTCRAANGGN GGCAT

25

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: one-of(11, 14, 20)
- (D) OTHER INFORMATION: /mod_base= OTHER

/note= "N = A or C or G or T"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 23
- (D) OTHER INFORMATION: /mod_base= OTHER

/note= "R = A or G"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CGGGATCCAA NGGNGGCATN CCRT

24

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATCACGACAC CACCAGAGCT GTTA

24

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CGAATTCAGA TCGTGAACGG GA

22

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CGAATTCAGG CGCTAGCAAT G

21

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAAAGGCGTA GAACCGA

17

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GCTGACCCAT TTCCTGTATC AGATAG

26

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GGAATTCTTC TGCTTGGCGA AT

22

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGGAATTCGA GGTTCTATAC ATAT

24

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CTGTGTGAAT GGAATCTGTG ATGTG

25

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TATCCCGGGT CATATGAGTC TCCTAGCC

28

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met Leu Gln Gln Pro Ser Gly Ser Thr Pro Ser Asn Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Ala Asp Thr Ala Leu Asn His Asp Phe Phe Trp Thr Asp Pro Met Pro
1 5 10 15

Ser

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Leu Gln Gln Pro
1 5

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Asn His Asp Phe Phe Trp Thr
1 5

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Ser Pro Glu Trp Pro Asp Ile
1 5

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Trp Tyr Phe Ser Asn Asp Gln Leu Ala Asn Ser Pro Ser Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Thr Val His Gly Met Pro Pro Phe Glu Gln Gln Leu Pro Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid

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- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Trp Tyr Phe Ser Asn Asp
1 5

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Pro Pro Phe Glu Gln
1 5

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

His Gly Met Pro Pro Phe
1 5

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GCAGGATCCA GAATTCCATA TGGCAAAGCA GTACGACTCG G

41

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CAGTACTCGA GTTATCAGAA GACGCGCTCA AAC

33

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4528 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```

GGGGGGGGGG GGGTGAATGA AGGAGCGGGC GGAGGAGGAA TTGTCATGGC GTCGGGCCGT      60
GGAGCTTCTT CTCGCTGGTT CTTTACTCGG GAACAGCTGG AGAACACGCC GAGCCGCCGC      120
TGCGGAGTGG AGGCGGATAA AGAGCTCTCG TGCCGCCAGC AGGCGGCCAA CCTCATCCAG      180
GAGATGGGAC AGCGTCTCAA TGTCTCTCAG CTTACAATAA AACTGCGAT TGTTTATATG      240
CACAGGTTTT ATATGCACCA TTCTTTCACC AAATTCAACA AAAATATAAT ATCGTCTACT      300
GCATTATTTT TGGCTGCAAA AGTGAAGAA CAGGCTCGAA AACTTGAACA TGTTATCAAA      360
GTAGCACATG CTTGTCTTCA TCCTCTAGAG CCACTGCTGG ATACTAAATG TGATGCTTAC      420
CTTCAACAGA CTCAAGAACT GGTTATACTT GAAACCATAA TGCTACAAAC TCTAGGTTTT      480
GAGATCACCA TTGAACACCC ACACACAGAT GTGGTGAAAT GTACCCAGTT AGTAAGAGCA      540
AGCAAGGATT TGGCACAGAC ATCCTATTTC ATGGCTACCA ACAGTCTGCA TCTTACAACC      600
TTCTGTCTTC AGTACAAACC AACAGTGATA GCATGTGTAT GCATTCATTT GGCTTGCAAA      660
TGGTCCAATT GGGAGATCCC TGTATCAACT GATGGAAAGC ATTGGTGGGA ATATGTGGAT      720
CCTACAGTTA CTCTAGAATT ATTAGATGAG CTAACACATG AGTTTCTACA AATATTGGAG      780
AAAACGCCTA ATAGGTTGAA GAAGATTCGA AACTGGAGGG CTAATCAGGC AGCTAGGAAA      840
CCAAAAGTAG ATGGACAGGT ATCAGAGACA CCACTTCTTG GTTCATCTTT GGTCCAGAAT      900
TCCATTTTAG TAGATAGTGT CACTGGTGTG CCTACAAACC CAAGTTTTCA GAAACCATCT      960
ACATCAGCAT TCCCTGCGCC AGTACCTCTA AATTCAGGAA ATATTTCTGT TCAAGACAGC     1020
CATACATCTG ATAATTTGTC AATGCTAGCA ACAGGAATGC CAAGTACTTC ATACGGTTTA     1080
TCATCACACC AGGAATGGCC TCAACATCAA GACTCAGCAA GGACAGAACA GCTATATTCA     1140
CAGAAACAGG AGACATCTTT GTCTGGTAGC CAGTACAACA TCAACTTCCA GCAGGGACCT     1200
TCTATATCAC TGCATTCAGG ATTACATCAC AGACCTGACA AAATTTCAGA TCATTCTTCT     1260
GTTAAGCAAG AATATACTCA TAAAGCAGGG AGCAGTAAAC ACCATGGGCC AATTTCCACT     1320
ACTCCAGGAA TAATTCCTCA GAAAATGTCT TTAGATAAAT ATAGAGAAAA GCGTAAACTA     1380
GAAACTCTTG ATCTCGATGT AAGGGATCAT TATATAGCTG CCCAGGTAGA ACAGCAGCAC     1440
AAACAAGGGC AGTCACAGGC AGCCAGCAGC AGTTCTGTTA CTTCTCCCAT TAAAATGAAA     1500
ATACCTATCG CAAATACTGA AAAATACATG GCAGATAAAA AGGAAAAGAG TGGGTCACTG     1560
AAATTACGGA TTCCAATACC ACCCACTGAT AAAAGCGCCA GTAAAGAAGA ACTGAAAATG     1620

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AAAATAAAAG	TTTCTTCTTC	AGAAAGACAC	AGCTCTTCTG	ATGAAGGCAG	TGGGAAAAGC	1680
AAACATTCAA	GCCCACATAT	TAGCAGAGAC	CATAAGGAGA	AGCACAAGGA	GCATCCTTCA	1740
AGCCGCCACC	ACACCAGCAG	CCACAAGCAT	TCCCCTCGC	ATAGTGGCAG	CAGCAGCGGT	1800
GGCAGTAAAC	ACAGTGCCGA	CGGAATACCA	CCCCTGTTC	TGAGGAGTCC	TGTTGGCCTG	1860
AGCAGTGATG	GCATTTCTTC	TAGCTCCAGC	TCTTCAAGGA	AGAGGCTGCA	TGTCAATGAT	1920
GCATCTCACA	ACCACCACTC	CAAAATGAGC	AAAAGTTCCA	AAAGTTCAGG	TGGGCTACGG	1980
ACATCTCAGC	ACCTCGTGAA	ACTGGACAAG	AAGCCAGTGG	AGACCAACGG	TCCTGATGCC	2040
AATCACGAGT	ACAGTACAAG	CAGCCAGCAT	ATGGACTACA	AAGACACATT	CGACATGCTG	2100
GACTCACTGT	TAAGTGCCCA	AGGAATGAAC	ATGTAATAAT	TTGTTTAGGT	CAATTTTTCC	2160
TTTACTTTTT	TAATTTAAAA	ATTGTTAGAA	TGGAAAAATT	CCTTCTGATC	TAGCAGTGGT	2220
AACCCCTGCT	GTTGCTGCCA	CTGCTTCAAT	ATTTGTAAGT	GCTACTTTAT	TCTTCATTCT	2280
GAAAAGAAGA	GATTATAGTA	AACAAGTCTT	TATCTCCACA	TATGATAGTG	TTATAAATAC	2340
TGTAAAGGCA	TGGAAGGTGC	AAAACTCAGT	ATTTCTACAA	TTGCAGCTAA	GAACATTAGG	2400
ATGAATGGCT	GGCTGCTTCT	AGGAATATAA	GATGCCTCAA	GCATTCATTA	TTTATGATTT	2460
GAATACTGTA	GCTATTTTTT	GTTGCTTGGC	TTTTGAATGA	GTGTAAATTG	TTTTCTTTTG	2520
TGTATTTATA	CTTGATGTGA	TGATTTGCAT	GTTTCAATGA	TAAAGGGATA	AAACAGTATA	2580
CTGACAACCTG	TTTACAAGAA	AGTGGAGAAA	ATGTACTACA	TTTTGTATGT	TTAGATATTA	2640
CCGTAAATAC	TCAGGATTGG	AGCTGCTTGT	AAGTATAACA	ATATACAGAA	TACTTTATTT	2700
TATCTTGTC	GAGTTCCATC	ACTATCTAAA	ACAAAGGTGC	AATTTTTTAT	GTTAACCTTA	2760
AATCTAGCCC	TTACTGGAAG	CCACTGATAG	GGACATTAC	TACCAGATGT	GTGCAGTGCA	2820
GCAGATGGTC	ATATAACACT	GTGAGGCACT	GAATTTTGCC	TTGAGAGGTT	CTGACCAGAT	2880
TGGCTGCTGA	AATAGCCCCT	AACTTTCTGA	AGGCTTGAAG	AGGAAAAAAT	AAAGTTTACA	2940
TACTCTTGAT	GGAAGTGCAT	TTAAATGTTT	GTTGGCTTGT	TGCAGTTCTA	TGAAACAGAG	3000
CTGTTAATAA	TGGTTATGTG	GATTACTGTG	ATTTGAAAAC	TAAATTCACA	ATAACTTACC	3060
TAGTAGAGAT	TTAGTGAGTT	GTTTCCTTTA	AAGAATTTTA	CACTACATAT	TTTAATAGTA	3120
AACAGGGTCA	CTTTCCTTTA	GCATTCAGAA	TGACACCATA	TTCTTAAATA	TACTCCTTCC	3180
CTGAAGCGTG	TTTGTGTGTG	ATGCCATATT	TCTTTTTTCT	GTAAATGTAG	TCTTCCTTAT	3240
AAAAATGAAA	TTAAACCTAT	GCTCTCAATT	CTTTTATATT	CTAACAATAA	ATAAAAAAGA	3300
AAAGATTACT	GACTGTGCAT	TGTACCTGTA	TTTATAGTTT	ATGGTTATCA	GAAGCTCTGT	3360
AAGAAAGAAA	AGGTCAGCTC	CCAGGCAAAC	CAGTAGTGGA	GGTTTTACAT	TTGTTTGCAC	3420
ATCTCAGTAT	ATTTCTGTTG	AGGTAAAGTT	TGCACAGTCA	TCTGACTTCT	GATCAAGCAT	3480

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TAGATTTTAA CTTGTTTAGA TTTTGTCTTA AACACCAGTA ATATGGCTCT TGTATTATCAG	3540
CTAATCTTGA ATTTATTCTG TGGTAAATCT TTTGAGTTGC TGAGTATATT TGAGATTGAT	3600
TGGATTCAAC CTCTTGTTGA ACTGAAAACCT TAATTTTTTTC TCTGTATTTT TGTTACAAAG	3660
CCACTGATAC GTGCACAATT GTAATTAAGT ATGTTGCAGT TGTAATATATT AGAGTTTAAT	3720
CTCATGCTCT ACCTTTATTT AGCAATTACC TAATTTGCCA GTAGCTTTAT AATTTTTTAAA	3780
GATAATTGTT CATTATTTTG TCAATGTTAT TTGAACTTGG GGTACTTAGG AGCCTCTTTG	3840
TAGGGACTGT GCCTAGGTAG CATGTCCTAA CATTTGTTCT GGTCTTGCAT AACTTCAGTA	3900
TCTTTGTCAT TATATGTAAC TTTGTTGCTC TGTATGGCAT AATATTGTAT CCATAAACAT	3960
GGTAATTTTG ATACAGTTAT ACTTTTACAG TGGTACATAA TCCAAGGACT AGTATAGAAT	4020
TAAGCTGAGT GCAAGATGAG GGAGGGAAGG GCTTTCTTGG TAATTTAGAT GTGAAACCTC	4080
TACAGAGCTA TCATGTAAAA ACTACATGAG GTGGTTGTGC TACTGTATAA TTGGGGGTGA	4140
TAATACCAGG AATTTTAATA AGATTTTGTA AAGAATATCC AGAAAAGTAG TGAACCTATT	4200
TTCAGTAGGC ATAGAAAACA ATGTGAATAT TTAAGGTCTG TGAATATAGT TAAACTTCAC	4260
TAAGAATTTG CAGAATTGTT TTGAGATGTG TGAATAAAGG TAATTTTATT GAATCTTCAT	4320
TGGTGCTAAT GTTGGACAGT TAAAAAGATA GCTAGTGTAT ATTGTTATGG GTCAGTACTT	4380
ATTAGTACTT CCAAAATTGA ATTTGAAATG CTATGTATTC ACTTTTCACT CTGTAAATGT	4440
AATTCTTTAC AATGACTTTA TTTATTAAAG GGCAGCCAGT TGTCATTTGT AAAAAAAAAA	4500
AAAAAAAAAA AAAGCGGCCG CTGAATTC	4528

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2091 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ATGGCGTCGG GCCGTGGAGC TTCTTCTCGC TGGTTCTTTA CTCGGGAACA GCTGGAGAAC	60
ACGCCGAGCC GCCGCTGCGG AGTGGAGGCG GATAAAGAGC TCTCGTGCCG CCAGCAGGCG	120
GCCAACCTCA TCCAGGAGAT GGGACAGCGT CTCAATGTCT CTCAGCTTAC AATAAACACT	180
GCGATTGTTT ATATGCACAG GTTTTATATG CACCATTCTT TCACCAAATT CAACAAAAAT	240
ATAATATCGT CTAATGCATT ATTTTGGCT GCAAAAGTGG AAGAACAGGC TCGAAAACCT	300
GAACATGTTA TCAAAGTAGC ACATGCTTGT CTTATCCTC TAGAGCCACT GCTGGATACT	360
AAATGTGATG CTTACCTTCA ACAGACTCAA GAACTGGTTA TACTTGAAAC CATAATGCTA	420
CAAACTCTAG GTTTTGAGAT CACCATTGAA CACCCACACA CAGATGTGGT GAAATGTACC	480

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CAGTTAGTAA GAGCAAGCAA GGATTTGGCA CAGACATCCT ATTTTCATGGC TACCAACAGT	540
CTGCATCTTA CAACCTTCTG TCTTCAGTAC AAACCAACAG TGATAGCATG TGTATGCATT	600
CATTTGGCTT GCAAATGGTC CAATTGGGAG ATCCCTGTAT CAACTGATGG AAAGCATTGG	660
TGGGAATATG TGGATCCTAC AGTTACTCTA GAATTATTAG ATGAGCTAAC ACATGAGTTT	720
CTACAAATAT TGGAGAAAAC GCCTAATAGG TTGAAGAAGA TTCGAAACTG GAGGGCTAAT	780
CAGGCAGCTA GGAAACCAAA AGTAGATGGA CAGGTATCAG AGACACCACT TCTTGGTTCA	840
TCTTTGGTCC AGAATTCCAT TTTAGTAGAT AGTGTCACTG GTGTGCCTAC AAACCCAAGT	900
TTTCAGAAAC CATCTACATC AGCATTCCCT GCGCCAGTAC CTCTAAATTC AGGAAATATT	960
TCTGTTCAAG ACAGCCATAC ATCTGATAAT TTGTCAATGC TAGCAACAGG AATGCCAAGT	1020
ACTTCATACG GTTTATCATC ACACCAGGAA TGGCCTCAAC ATCAAGACTC AGCAAGGACA	1080
GAACAGCTAT ATTCACAGAA ACAGGAGACA TCTTTGTCTG GTAGCCAGTA CAACATCAAC	1140
TTCCAGCAGG GACCTTCTAT ATCACTGCAT TCAGGATTAC ATCACAGACC TGACAAAATT	1200
TCAGATCATT CTTCTGTAA GCAAGAATAT ACTCATAAAG CAGGGAGCAG TAAACACCAT	1260
GGGCCAATTT CCACTACTCC AGGAATAATT CCTCAGAAAA TGTCTTTAGA TAAATATAGA	1320
GAAAAGCGTA AACTAGAAAC TCTTGATCTC GATGTAAGGG ATCATTATAT AGCTGCCCAG	1380
GTAGAACAGC AGCACAAACA AGGGCAGTCA CAGGCAGCCA GCAGCAGTTC TGTTACTTCT	1440
CCCATTAATA TGAAAATACC TATCGCAAAT ACTGAAAAAT ACATGGCAGA TAAAAAGGAA	1500
AAGAGTGGGT CACTGAAATT ACGGATTCCA ATACCACCCA CTGATAAAAG CGCCAGTAAA	1560
GAAGAACTGA AAATGAAAAT AAAAGTTTCT TCTTCAGAAA GACACAGCTC TTCTGATGAA	1620
GGCAGTGGGA AAAGCAAACA TTCAAGCCCA CATATTAGCA GAGACCATAA GGAGAAGCAC	1680
AAGGAGCATC CTTCAAGCCG CCACCACACC AGCAGCCACA AGCATTCCCA CTCGCATAGT	1740
GGCAGCAGCA GCGGTGGCAG TAAACACAGT GCCGACGGAA TACCACCCAC TGTTCTGAGG	1800
AGTCCTGTTG GCCTGAGCAG TGATGGCATT TCCTCTAGCT CCAGCTCTTC AAGGAAGAGG	1860
CTGCATGTCA ATGATGCATC TCACAACCAC CACTCAGAAA TGAGCAAAAG TTCCAAAAGT	1920
TCAGGTGGGC TACGGACATC TCAGCACCTC GTGAAACTGG ACAAGAAGCC AGTGGAGACC	1980
AACGGTCCTG ATGCCAATCA CGAGTACAGT ACAAGCAGCC AGCATATGGA CTACAAAGAC	2040
ACATTCGACA TGCTGGACTC ACTGTTAAGT GCCCAAGGAA TGAACATGTA A	2091

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 696 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

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Met Ala Ser Gly Arg Gly Ala Ser Ser Arg Trp Phe Phe Thr Arg Glu
1      5      10
Gln Leu Glu Asn Thr Pro Ser Arg Arg Cys Gly Val Glu Ala Asp Lys
20     25     30
Glu Leu Ser Cys Arg Gln Gln Ala Ala Asn Leu Ile Gln Glu Met Gly
35     40     45
Gln Arg Leu Asn Val Ser Gln Leu Thr Ile Asn Thr Ala Ile Val Tyr
50     55     60
Met His Arg Phe Tyr Met His His Ser Phe Thr Lys Phe Asn Lys Asn
65     70     75     80
Ile Ile Ser Ser Thr Ala Leu Phe Leu Ala Ala Lys Val Glu Glu Gln
85     90     95
Ala Arg Lys Leu Glu His Val Ile Lys Val Ala His Ala Cys Leu His
100    105    110
Pro Leu Glu Pro Leu Leu Asp Thr Lys Cys Asp Ala Tyr Leu Gln Gln
115    120    125
Thr Gln Glu Leu Val Ile Leu Glu Thr Ile Met Leu Gln Thr Leu Gly
130    135    140
Phe Glu Ile Thr Ile Glu His Pro His Thr Asp Val Val Lys Cys Thr
145    150    155    160
Gln Leu Val Arg Ala Ser Lys Asp Leu Ala Gln Thr Ser Tyr Phe Met
165    170    175
Ala Thr Asn Ser Leu His Leu Thr Thr Phe Cys Leu Gln Tyr Lys Pro
180    185
Thr Val Ile Ala Cys Val Cys Ile His Leu Ala Cys Lys Trp Ser Asn
195    200    205
Trp Glu Ile Pro Val Ser Thr Asp Gly Lys His Trp Trp Glu Tyr Val
210    215    220
Asp Pro Thr Val Thr Leu Glu Leu Leu Asp Glu Leu Thr His Glu Phe
225    230    235    240
Leu Gln Ile Leu Glu Lys Thr Pro Asn Arg Leu Lys Lys Ile Arg Asn
245    250    255
Trp Arg Ala Asn Gln Ala Ala Arg Lys Pro Lys Val Asp Gly Gln Val
260    265    270
Ser Glu Thr Pro Leu Leu Gly Ser Ser Leu Val Gln Asn Ser Ile Leu
275    280    285
Val Asp Ser Val Thr Gly Val Pro Thr Asn Pro Ser Phe Gln Lys Pro
290    295    300
Ser Thr Ser Ala Phe Pro Ala Pro Val Pro Leu Asn Ser Gly Asn Ile
305    310    315    320
Ser Val Gln Asp Ser His Thr Ser Asp Asn Leu Ser Met Leu Ala Thr

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325

330

335

Gly Met Pro Ser Thr Ser Tyr Gly Leu Ser Ser His Gln Glu Trp Pro
 340 345 350
 Gln His Gln Asp Ser Ala Arg Thr Glu Gln Leu Tyr Ser Gln Lys Gln
 355 360 365
 Glu Thr Ser Leu Ser Gly Ser Gln Tyr Asn Ile Asn Phe Gln Gln Gly
 370 375 380
 Pro Ser Ile Ser Leu His Ser Gly Leu His His Arg Pro Asp Lys Ile
 385 390 395 400
 Ser Asp His Ser Ser Val Lys Gln Glu Tyr Thr His Lys Ala Gly Ser
 405 410 415
 Ser Lys His His Gly Pro Ile Ser Thr Thr Pro Gly Ile Ile Pro Gln
 420 425 430
 Lys Met Ser Leu Asp Lys Tyr Arg Glu Lys Arg Lys Leu Glu Thr Leu
 435 440 445
 Asp Leu Asp Val Arg Asp His Tyr Ile Ala Ala Gln Val Glu Gln Gln
 450 455 460
 His Lys Gln Gly Gln Ser Gln Ala Ala Ser Ser Ser Ser Val Thr Ser
 465 470 475 480
 Pro Ile Lys Met Lys Ile Pro Ile Ala Asn Thr Glu Lys Tyr Met Ala
 485 490 495
 Asp Lys Lys Glu Lys Ser Gly Ser Leu Lys Leu Arg Ile Pro Ile Pro
 500 505 510
 Pro Thr Asp Lys Ser Ala Ser Lys Glu Glu Leu Lys Met Lys Ile Lys
 515 520 525
 Val Ser Ser Ser Glu Arg His Ser Ser Ser Asp Glu Gly Ser Gly Lys
 530 535 540
 Ser Lys His Ser Ser Pro His Ile Ser Arg Asp His Lys Glu Lys His
 545 550 555 560
 Lys Glu His Pro Ser Arg His His Thr Ser Ser His Lys His Ser
 565 570 575
 His Ser His Ser Gly Ser Ser Ser Gly Gly Ser Lys His Ser Ala Asp
 580 585 590
 Gly Ile Pro Pro Thr Val Leu Arg Ser Pro Val Gly Leu Ser Ser Asp
 595 600 605
 Gly Ile Ser Ser Ser Ser Ser Ser Ser Arg Lys Arg Leu His Val Asn
 610 615 620
 Asp Ala Ser His Asn His His Ser Lys Met Ser Lys Ser Ser Lys Ser
 625 630 635 640
 Ser Gly Gly Leu Arg Thr Ser Gln His Leu Val Lys Leu Asp Lys Lys
 645 650 655
 Pro Val Glu Thr Asn Gly Pro Asp Ala Asn His Glu Tyr Ser Thr Ser

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660	665	670
Ser Gln His Met Asp Tyr Lys	Asp Thr Phe Asp Met	Leu Asp Ser Leu
675	680	685
Leu Ser Ala Gln Gly Met Asn Met		
690	695	

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2190 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ATGGCGTCTGG GCCGTGGAGC TTCTTCTCGC TGGTTCTTTA CTCGGGAACA GCTGGAGAAC	60
ACGCCGAGCC GCCGCTGCGG AGTGGAGGCG GATAAAGAGC TCTCGTGCCG CCAGCAGGCG	120
GCCAACCTCA TCCAGGAGAT GGGACAGCGT CTCAATGTCT CTCAGCTTAC AATAAACT	180
GCGATTGTTT ATATGCACAG GTTTTATATG CACCATTCTT TCACCAAATT CAACAAAAT	240
ATAATATCGT CTA CTG CATT ATTTTGGCT GCAAAAGTGG AAGAACAGGC TCGAAACTT	300
GAACATGTTA TCAAAGTAGC ACATGCTTGT CTTTCATCTC TAGAGCCACT GCTGGATACT	360
AAATGTGATG CTTACCTTCA ACAGACTCAA GAACTGGTTA TACTTGAAAC CATAATGCTA	420
CAAACTCTAG GTTTTGAGAT CACCATTGAA CACCCACACA CAGATGTGGT GAAATGTACC	480
CAGTTAGTAA GAGCAAGCAA GGATTTGGCA CAGACATCCT ATTTTCATGGC TACCAACAGT	540
CTGCATCTTA CAACCTTCTG TCTTCAGTAC AAACCAACAG TGATAGCATG TGTATGCATT	600
CATTTGGCTT GCAAATGGTC CAATTGGGAG ATCCCTGTAT CAACTGATGG AAAGCATTGG	660
TGGGAATATG TGGATCCTAC AGTTACTCTA GAATTATTAG ATGAGCTAAC ACATGAGTTT	720
CTACAAATAT TGGAGAAAAC GCCTAATAGG TTGAAGAAGA TTCGAACTG GAGGGCTAAT	780
CAGGCAGCTA GGAAACCAAA AGTAGATGGA CAGGTATCAG AGACACCACT TCTTGGTTCA	840
TCTTTGGTCC AGAATTCCAT TTTAGTAGAT AGTGTCACTG GTGTGCCTAC AAACCCAAGT	900
TTTCAGAAAC CATCTACATC AGCATTCCCT GCGCCAGTAC CTCTAAATTC AGGAAATATT	960
TCTGTTCAAG ACAGCCATAC ATCTGATAAT TTGTCAATGC TAGCAACAGG AATGCCAAGT	1020
ACTTCATACG GTTTATCATC ACACCAGGAA TGGCCTCAAC ATCAAGACTC AGCAAGGACA	1080
GAACAGCTAT ATTCACAGAA ACAGGAGACA TCTTTGTCTG GTAGCCAGTA CAACATCAAC	1140
TTCCAGCAGG GACCTTCTAT ATCACTGCAT TCAGGATTAC ATCACAGACC TGACAAAATT	1200
TCAGATCATT CTTCTGTAA GCAGGAATAT ACTCATAAAG CAGGGAGCAG TAAACACCAT	1260
GGGCCAATTT CCACTACTCC AGGAATAATT CCTCAGAAAA TGTCTTTAGA TAAATATAGA	1320

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GAAAAGCGTA AACTAGAAAC TCTTGATCTC GATGTAAGGG ATCATTATAT AGCTGCCCAG	1380
GTAGAACAGC AGCACAAACA AGGGCAGTCA CAGGCAGCCA GCAGCAGTTC TGTTACTTCT	1440
CCCATTAAAA TGAAAATACC TATCGCAAAT ACTGAAAAAT ACATGGCAGA TAAAAAGGAA	1500
AAGAGTGGGT CACTGAAATT ACGGATTCCA ATACCACCCA CTGATAAAAG CGCCAGTAAA	1560
GAAGAACTGA AAATGAAAAT AAAAGTTTCT TCTTCAGAAA GACACAGCTC TTCTGATGAA	1620
GGCAGTGGGA AAAGCAAACA TTCAAGCCCA CATATTAGCA GAGACCATAA GGAGAAGCAC	1680
AAGGAGCATC CTTCAAGCCG CCACCACACC AGCAGCCACA AGCATTCCCA CTCGCATAGT	1740
GGCAGCAGCA GCGGTGGCAG TAAACACAGT GCCGACGGAA TACCACCCAC TGTTCTGAGG	1800
AGTCCTGTTG GCCTGAGCAG TGATGGCATT TCCTCTAGCT CCAGCTCTTC AAGGAAGAGG	1860
CTGCATGTCA ATGATGCATC TCACAACCAC CACTCCAAAA TGAGCAAAAG TTCCAAAAGT	1920
TCAGGTAGTT CATCTAGTTC TTCCTCCTCT GTTAAGCAGT ATATATCCTC TCACAACTCT	1980
GTTTTTAACC ATCCCTTACC CCTCCTCCCC TGTCACATAC CAGGTGGGCT ACGGACATCT	2040
CTGCACCTCG TGAAACTGGA CAAGAAGCCA GTGGAGACCA ACGGTCCTGA TGCCAATCAC	2100
GAGTACAGTA CAAGCAGCCA GCATATGGAC TACAAAGACA CATTGACAT GCTGGACTCA	2160
CTGTTAAGTG CCAAGGAAT GAACATGTAA	2190

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Met	Ala	Ser	Gly	Arg	Gly	Ala	Ser	Ser	Arg	Trp	Phe	Phe	Thr	Arg	Glu
1				5					10					15	
Gln	Leu	Glu	Asn	Thr	Pro	Ser	Arg	Arg	Cys	Gly	Val	Glu	Ala	Asp	Lys
			20					25					30		
Glu	Leu	Ser	Cys	Arg	Gln	Gln	Ala	Ala	Asn	Leu	Ile	Gln	Glu	Met	Gly
		35					40					45			
Gln	Arg	Leu	Asn	Val	Ser	Gln	Leu	Thr	Ile	Asn	Thr	Ala	Ile	Val	Tyr
	50					55					60				
Met	His	Arg	Phe	Tyr	Met	His	His	Ser	Phe	Thr	Lys	Phe	Asn	Lys	Asn
65					70					75				80	
Ile	Ile	Ser	Ser	Thr	Ala	Leu	Phe	Leu	Ala	Ala	Lys	Val	Glu	Glu	Gln
			85					90					95		
Ala	Arg	Lys	Leu	Glu	His	Val	Ile	Lys	Val	Ala	His	Ala	Cys	Leu	His
		100						105					110		
Pro	Leu	Glu	Pro	Leu	Leu	Asp	Thr	Lys	Cys	Asp	Ala	Tyr	Leu	Gln	Gln

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115

120

125

Thr Gln Glu Leu Val Ile Leu Glu Thr Ile Met Leu Gln Thr Leu Gly
 130 135 140
 Phe Glu Ile Thr Ile Glu His Pro His Thr Asp Val Val Lys Cys Thr
 145 150 155 160
 Gln Leu Val Arg Ala Ser Lys Asp Leu Ala Gln Thr Ser Tyr Phe Met
 165 170 175
 Ala Thr Asn Ser Leu His Leu Thr Thr Phe Cys Leu Gln Tyr Lys Pro
 180 185 190
 Thr Val Ile Ala Cys Val Cys Ile His Leu Ala Cys Lys Trp Ser Asn
 195 200 205
 Trp Glu Ile Pro Val Ser Thr Asp Gly Lys His Trp Trp Glu Tyr Val
 210 215 220
 Asp Pro Thr Val Thr Leu Glu Leu Leu Asp Glu Leu Thr His Glu Phe
 225 230 235 240
 Leu Gln Ile Leu Glu Lys Thr Pro Asn Arg Leu Lys Lys Ile Arg Asn
 245 250 255
 Trp Arg Ala Asn Gln Ala Ala Arg Lys Pro Lys Val Asp Gly Gln Val
 260 265 270
 Ser Glu Thr Pro Leu Leu Gly Ser Ser Leu Val Gln Asn Ser Ile Leu
 275 280 285
 Val Asp Ser Val Thr Gly Val Pro Thr Asn Pro Ser Phe Gln Lys Pro
 290 295 300
 Ser Thr Ser Ala Phe Pro Ala Pro Val Pro Leu Asn Ser Gly Asn Ile
 305 310 315 320
 Ser Val Gln Asp Ser His Thr Ser Asp Asn Leu Ser Met Leu Ala Thr
 325 330 335
 Gly Met Pro Ser Thr Ser Tyr Gly Leu Ser Ser His Gln Glu Trp Pro
 340 345 350
 Gln His Gln Asp Ser Ala Arg Thr Glu Gln Leu Tyr Ser Gln Lys Gln
 355 360 365
 Glu Thr Ser Leu Ser Gly Ser Gln Tyr Asn Ile Asn Phe Gln Gln Gly
 370 375 380
 Pro Ser Ile Ser Leu His Ser Gly Leu His His Arg Pro Asp Lys Ile
 385 390 395 400
 Ser Asp His Ser Ser Val Lys Gln Glu Tyr Thr His Lys Ala Gly Ser
 405 410 415
 Ser Lys His His Gly Pro Ile Ser Thr Thr Pro Gly Ile Ile Pro Gln
 420 425 430
 Lys Met Ser Leu Asp Lys Tyr Arg Glu Lys Arg Lys Leu Glu Thr Leu
 435 440 445
 Asp Leu Asp Val Arg Asp His Tyr Ile Ala Ala Gln Val Glu Gln Gln

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450		455		460
His 465	Lys Gln Gly Gln Ser 470	Gln Ala Ala Ser Ser 475	Ser Ser Val Thr Ser 480	
Pro Ile Lys Met 485	Lys Ile Pro Ile Ala Asn 490	Thr Glu Lys Tyr Met 495	Ala	
Asp Lys Lys Glu 500	Lys Ser Gly Ser Leu 505	Leu Arg Ile Pro 510	Ile Pro	
Pro Thr Asp 515	Lys Ser Ala Ser Lys 520	Glu Glu Leu Lys Met 525	Lys Ile Lys	
Val Ser Ser Ser 530	Glu Arg His Ser Ser Ser 535	Asp Glu Gly Ser Gly Lys 540		
Ser Lys His Ser Ser 545	Pro His Ile Ser Arg Asp 555	His Lys Glu Lys His 560		
Lys Glu His Pro Ser 565	Ser Arg His His Thr Ser Ser His Lys His 575	Ser		
His Ser His Ser 580	Gly Ser Ser Ser Gly 585	Gly Ser Lys His Ser Ala Asp 590		
Gly Ile Pro Pro Thr Val 595	Leu Arg Ser Pro Val Gly Leu Ser Ser Asp 605			
Gly Ile Ser Ser Ser Ser 610	Ser Ser Ser Arg Lys Arg 620	Leu His Val Asn		
Asp Ala Ser His Asn His 625	His Ser Lys Met Ser 635	Lys Ser Ser Lys Ser 640		
Ser Gly Ser Ser Ser 645	Ser Ser Ser Ser Ser 650	Val Lys Gln Tyr Ile Ser 655		
Ser His Asn Ser Val Phe Asn His 660	Pro Leu Pro Leu Leu Pro Cys His 670			
Ile Pro Gly Gly Leu Arg Thr 675	Ser Gln His Leu Val Lys 685	Leu Asp Lys		
Lys Pro Val Glu Thr Asn Gly 690	Pro Asp Ala Asn His 700	Glu Tyr Ser Thr		
Ser Ser Gln His Met Asp 705	Tyr Lys Asp Thr Phe 715	Asp Met Leu Asp Ser 720		
Leu Leu Ser Ala Gln Gly Met Asn Met 725				

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GGAAGTGCCT	GCAACCTTCG	CCGCTGCCTT	CTGGTTGAAG	CACTATGGAG	GGAGAGAGGA	60
AGAACAACAA	CAAACGGTGG	TATTTCACTC	GAGAACAGCT	GGAAAATAGC	CCATCCCGTC	120
GTTTTGGCGT	GGACCCAGAT	AAAGAACTTT	CTTATCGCCA	GCAGGCGGCC	AATCTGCTTC	180
AGGACATGGG	GCAGCGTCTT	AACGTCTCAC	AATTGACTAT	CAACACTGCT	ATAGTATACA	240
TGCATCGATT	CTACATGATT	CAGTCCTTCA	CACGGTTCCC	TGGAAATTCT	GTGGCTCCAG	300
CAGCCTTGTT	TCTAGCAGCT	AAAGTGGAGG	AGCAGCCCAA	AAAATTGGAA	CATGTCATCA	360
AGGTAGCACA	TACTTGCTC	CATCCTCAGG	AATCCCTTCC	TGATACTAGA	AGTGAGGCTT	420
ATTTGCAACA	AGTTCAAGAT	CTGGTCATTT	TAGAAAGCAT	AATTTTGCAG	ACTTTAGGCT	480
TTGAACTAAC	AATTGATCAC	CCACATACTC	ATGTAGTAAA	GTGCACTCAA	CTTGTTTCGAG	540
CAAGCAAGGA	CTTAGCACAG	ACTTCTTACT	TCATGGCAAC	CAACAGCCTG	CATTTGACCA	600
CATTTAGCCT	GCAGTACACA	CCTCCTGTGG	TGGCCTGTGT	CTGCATTCAC	CTGGCTTGCA	660
AGTGGTCCAA	TTGGGAGATC	CCAGTCTCAA	CTGACGGGAA	GCACTGGTGG	GAGTATGTTG	720
ACGCCACTGT	GACCTTGGA	CTTTTAGATG	AACTGACACA	TGAGTTTCTA	CAGATTTTGG	780
AGAAACTCC	CAACAGGCTC	AAACGCATTT	GGAATTGGAG	GGCATGCGAG	GCTGCCAAGA	840
AAACAAAAGC	AGATGACCGA	GGAACAGATG	AAAAGACTTC	AGAGCAGACA	ATCCTCAATA	900
TGATTTCCCA	GAGCTCTTCA	GACACAACCA	TTGCAGGTTT	AATGAGCATG	TCAACTTCTA	960
CCACAAGTGC	AGTGCCTTCC	CTGCCAGTCT	CCGAAGAGTC	ATCCAGCAAC	TTAACCAGTG	1020
TGGAGATGTT	GCCGGGCAAG	CGTTGGCTGT	CCTCCCAACC	TTCTTTCAAA	CTAGAACCTA	1080
CTCAGGGTCA	TCGGACTAGT	GAGAATTTAG	CATTACAGG	AGTTGATCAT	TCCTTACCAC	1140
AGGATGGTTC	AAATGCATTT	ATTTCCCAGA	AGCAGAATAG	TAAGAGTGTG	CCATCAGCTA	1200
AAGTGTCACT	GAAAGAATAC	CGCGCGAAGC	ATGCAGAAGA	ATTGGCTGCC	CAGAAGAGGC	1260
AACTGGAGAA	CATGGAAGCC	AATGTGAAGT	CACAATATGC	ATATGCTGCC	CAGAATCTCC	1320
TTTCTCATCA	TGATAGCCAT	TCTTCAGTCA	TTCTAAAAAT	GCCCATAGAG	GGTTCAGAAA	1380
ACCCCGAGCG	GCCTTTTCTG	GAAAAGGCTG	ACAAAACAGC	TCTCAAAATG	AGAATCCCAG	1440
TGGCAGGTGG	AGATAAAGCT	GCGTCTTCAA	AACCAGAGGA	GATAAAAATG	CGCATAAAAG	1500
TCCATGCTGC	AGCTGATAAG	CACAATTCTG	TAGAGGACAG	TGTTACAAAG	AGCCGAGAGC	1560
ACAAAGAAGA	GCGCAAGACT	CACCCATCTA	ATCATCATCA	TCATCATAAT	CACCACTCAC	1620
ACAAGCACTC	TCATTCCCAA	CTTCCAGTTG	GTAAGGGGAA	CAAACGTCCT	GGTGATCCAA	1680
AACATAGTAG	CCAGACAAGC	AACTTAGCAC	ATAAAACCTA	TAGCTTGTCT	AGTTCTTTTT	1740
CCTCTTCCAG	TTCTACTCGT	AAAAGGGGAC	CCTCTGAAGA	GACTGGAGGG	GCTGTGTTTG	1800
ATCATCCAGC	CAAGATTGCC	AAGAGTACTA	AATCCTCTTC	CCTAAATTTT	TCCTTCCCTT	1860

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CACTTCCTAC AATGGGTCAG ATGCCTGGGC ATAGCTCAGA CACAAGTGGC CTTTCCTTTT	1920
CACAGCCCAG CTGTAAACT CGTGTCCCTC ATTCGAACT GGATAAAGGG CCCACTGGGG	1980
CCAATGGTCA CAACACGACC CAGACAATAG ACTATCAAGA CACTGTGAAT ATGCTTCACT	2040
CCCTGCTCAG TGCCCAGGGT GTTCAGCCCA CTCAGCCCAC TGCATTTGAA TTTGTTGTC	2100
CTTATAGTGA CTATCTGAAT CCTCGGTCTG GTGGAATCTC CTCGAGATCT GGCAATACAG	2160
ACAAACCCCG GCCACCACCT CTGCCATCAG AACCTCCTCC ACCACTTCCA CCCCTTCCTA	2220
AGTAAAAAAA GAAAAAGAAG AGGAGAAAAA AACTTCTTTA AAAAAACACA TAATTTTCT	2280
TTTTTTTTTG GGGAAAAAAA AATTTTTTTT AAAATTTTTT CCCCAAGGGA CGGGGGAAAA	2340
TTTTATTTTT AAAATTTTTT	2360

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2181 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

ATGGAGGGAG AGAGGAAGAA CAACAACAAA CGGTGGTATT TCACTCGAGA ACAGCTGGAA	60
AATAGCCCAT CCCGTCGTTT TGGCGTGGAC CCAGATAAAG AACTTTCTTA TCGCCAGCAG	120
GCGGCCAATC TGCTTCAGGA CATGGGGCAG CGTCTTAACG TCTCACAATT GACTATCAAC	180
ACTGCTATAG TATACATGCA TCGATTCTAC ATGATTCAGT CCTTCACACG GTTCCCTGGA	240
AATTCTGTGG CTCCAGCAGC CTTGTTTCTA GCAGCTAAAG TGGAGGAGCA GCCCAAAAAA	300
TTGGAACATG TCATCAAGGT AGCACATACT TGTCTCCATC CTCAGGAATC CCTTCCTGAT	360
ACTAGAAGTG AGGCTTATTT GCAACAAGTT CAAGATCTGG TCATTTTAGA AAGCATAATT	420
TTGCAGACTT TAGGCTTTGA ACTAACAATT GATCACCCAC ATACTCATGT AGTAAAGTGC	480
ACTCAACTTG TTCGAGCAAG CAAGGACTTA GCACAGACTT CTTACTTCAT GGCAACCAAC	540
AGCCTGCATT TGACCACATT TAGCCTGCAG TACACACCTC CTGTGGTGGC CTGTGTCTGC	600
ATTCACCTGG CTTGCAAGTG GTCCAATTGG GAGATCCCAG TCTCAACTGA CGGGAAGCAC	660
TGGTGGGAGT ATGTTGACGC CACTGTGACC TTGGAACCTT TAGATGAACT GACACATGAG	720
TTTCTACAGA TTTTGGAGAA AACTCCCAAC AGGCTCAAAC GCATTTGGAA TTGGAGGGCA	780
TGCGAGGCTG CCAAGAAAAC AAAAGCAGAT GACCGAGGAA CAGATGAAAA GACTTCAGAG	840
CAGACAATCC TCAATATGAT TTCCCAGAGC TCTTCAGACA CAACCATTGC AGGTTTAATG	900
AGCATGTCAA CTTCTACCAC AAGTGCAGTG CCTTCCCTGC CAGTCTCCGA AGAGTCATCC	960
AGCAACTTAA CCAGTGTGGA GATGTTGCCG GGCAAGCGTT GGCTGTCCTC CCAACCTTCT	1020

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TTCAAAC TAG AACCTACTCA GGGTCATCGG ACTAGTGAGA ATTTAGCACT TACAGGAGTT	1080
GATCATTCCT TACCACAGGA TGGTTCAAAT GCATTTATTT CCCAGAAGCA GAATAGTAAG	1140
AGTGTGCCAT CAGCTAAAGT GTCAGTGAAG GAATACCGCG CGAAGCATGC AGAAGAATTG	1200
GCTGCCCAGA AGAGGCAACT GGAGAACATG GAAGCCAATG TGAAGTCACA ATATGCATAT	1260
GCTGCCCAGA ATCTCCTTTC TCATCATGAT AGCCATTCTT CAGTCATTCT AAAAATGCCC	1320
ATAGAGGGTT CAGAAAACCC CGAGCGGCCT TTTCTGGAAA AGGCTGACAA AACAGCTCTC	1380
AAAATGAGAA TCCCAGTGGC AGGTGGAGAT AAAGCTGCGT CTTCAAAACC AGAGGAGATA	1440
AAAATGCGCA TAAAAGTCCA TGCTGCAGCT GATAAGCACA ATTCTGTAGA GGACAGTGTT	1500
ACAAAGAGCC GAGAGCACAA AGAAGAGCGC AAGACTCACC CATCTAATCA TCATCATCAT	1560
CATAATCACC ACTCACACAA GCACTCTCAT TCCCAACTTC CAGTTGGTAC TGGGAACAAA	1620
CGTCCTGGTG ATCCAAAACA TAGTAGCCAG ACAAGCAACT TAGCACATAA AACCTATAGC	1680
TTGTCTAGTT CTTTTCTCTC TTCCAGTTCT ACTCGTAAAA GGGGACCCTC TGAAGAGACT	1740
GGAGGGGCTG TGTTTGATCA TCCAGCCAAG ATTGCCAAGA GACTAAATC CTCTTCCCTA	1800
AATTTCTCCT TCCCTTCACT TCCTACAATG GGTCAGATGC CTGGGCATAG CTCAGACACA	1860
AGTGGCCTTT CTTTTTACA GCCCAGCTGT AAAACTCGTG TCCCTCATTC GAAACTGGAT	1920
AAAGGGCCCA CTGGGGCCAA TGGTCACAAC ACGACCCAGA CAATAGACTA TCAAGACT	1980
GTGAATATGC TTCACTCCCT GCTCAGTGCC CAGGGTGTTT AGCCCACTCA GCCCACTGCA	2040
TTTGAATTTG TTCGTCCTTA TAGTGACTAT CTGAATCCTC GGTCTGGTGG AATCTCCTCG	2100
AGATCTGGCA ATACAGACAA ACCCCGGCCA CCACCTCTGC CATCAGAACC TCCTCCACCA	2160
CTTCCACCCC TTCCTAAGTA A	2181

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 726 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met	Glu	Gly	Glu	Arg	Lys	Asn	Asn	Asn	Lys	Arg	Trp	Tyr	Phe	Thr	Arg
1				5					10					15	
Glu	Gln	Leu	Glu	Asn	Ser	Pro	Ser	Arg	Arg	Phe	Gly	Val	Asp	Pro	Asp
			20					25					30		
Lys	Glu	Leu	Ser	Tyr	Arg	Gln	Gln	Ala	Ala	Asn	Leu	Leu	Gln	Asp	Met
			35				40					45			
Gly	Gln	Arg	Leu	Asn	Val	Ser	Gln	Leu	Thr	Ile	Asn	Thr	Ala	Ile	Val
	50					55					60				

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Tyr	Met	His	Arg	Phe	Tyr	Met	Ile	Gln	Ser	Phe	Thr	Arg	Phe	Pro	Gly	65	70	75	80
Asn	Ser	Val	Ala	Pro	Ala	Ala	Leu	Phe	Leu	Ala	Ala	Lys	Val	Glu	Glu	85	90	95	
Gln	Pro	Lys	Lys	Leu	Glu	His	Val	Ile	Lys	Val	Ala	His	Thr	Cys	Leu	100	105	110	
His	Pro	Gln	Glu	Ser	Leu	Pro	Asp	Thr	Arg	Ser	Glu	Ala	Tyr	Leu	Gln	115	120	125	
Gln	Val	Gln	Asp	Leu	Val	Ile	Leu	Glu	Ser	Ile	Ile	Leu	Gln	Thr	Leu	130	135	140	
Gly	Phe	Glu	Leu	Thr	Ile	Asp	His	Pro	His	Thr	His	Val	Val	Lys	Cys	145	150	155	160
Thr	Gln	Leu	Val	Arg	Ala	Ser	Lys	Asp	Leu	Ala	Gln	Thr	Ser	Tyr	Phe	165	170	175	
Met	Ala	Thr	Asn	Ser	Leu	His	Leu	Thr	Thr	Phe	Ser	Leu	Gln	Tyr	Thr	180	185	190	
Pro	Pro	Val	Val	Ala	Cys	Val	Cys	Ile	His	Leu	Ala	Cys	Lys	Trp	Ser	195	200	205	
Asn	Trp	Glu	Ile	Pro	Val	Ser	Thr	Asp	Gly	Lys	His	Trp	Trp	Glu	Tyr	210	215	220	
Val	Asp	Ala	Thr	Val	Thr	Leu	Glu	Leu	Leu	Asp	Glu	Leu	Thr	His	Glu	225	230	235	240
Phe	Leu	Gln	Ile	Leu	Glu	Lys	Thr	Pro	Asn	Arg	Leu	Lys	Arg	Ile	Trp	245	250	255	
Asn	Trp	Arg	Ala	Cys	Glu	Ala	Ala	Lys	Lys	Thr	Lys	Ala	Asp	Asp	Arg	260	265	270	
Gly	Thr	Asp	Glu	Lys	Thr	Ser	Glu	Gln	Thr	Ile	Leu	Asn	Met	Ile	Ser	275	280	285	
Gln	Ser	Ser	Ser	Asp	Thr	Thr	Ile	Ala	Gly	Leu	Met	Ser	Met	Ser	Thr	290	295	300	
Ser	Thr	Thr	Ser	Ala	Val	Pro	Ser	Leu	Pro	Val	Ser	Glu	Glu	Ser	Ser	305	310	315	320
Ser	Asn	Leu	Thr	Ser	Val	Glu	Met	Leu	Pro	Gly	Lys	Arg	Trp	Leu	Ser	325	330	335	
Ser	Gln	Pro	Ser	Phe	Lys	Leu	Glu	Pro	Thr	Gln	Gly	His	Arg	Thr	Ser	340	345	350	
Glu	Asn	Leu	Ala	Leu	Thr	Gly	Val	Asp	His	Ser	Leu	Pro	Gln	Asp	Gly	355	360	365	
Ser	Asn	Ala	Phe	Ile	Ser	Gln	Lys	Gln	Asn	Ser	Lys	Ser	Val	Pro	Ser	370	375	380	
Ala	Lys	Val	Ser	Leu	Lys	Glu	Tyr	Arg	Ala	Lys	His	Ala	Glu	Glu	Leu	385	390	395	400

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Ala Ala Gln Lys Arg Gln Leu Glu Asn Met Glu Ala Asn Val Lys Ser
405 410 415

Gln Tyr Ala Tyr Ala Ala Gln Asn Leu Leu Ser His His Asp Ser His
420 425 430

Ser Ser Val Ile Leu Lys Met Pro Ile Glu Gly Ser Glu Asn Pro Glu
435 440 445

Arg Pro Phe Leu Glu Lys Ala Asp Lys Thr Ala Leu Lys Met Arg Ile
450 455 460

Pro Val Ala Gly Gly Asp Lys Ala Ala Ser Ser Lys Pro Glu Glu Ile
465 470 475 480

Lys Met Arg Ile Lys Val His Ala Ala Ala Asp Lys His Asn Ser Val
485 490 495

Glu Asp Ser Val Thr Lys Ser Arg Glu His Lys Glu Glu Arg Lys Thr
500 505 510

His Pro Ser Asn His His His His Asn His His Ser His Lys His
515 520 525

Ser His Ser Gln Leu Pro Val Gly Thr Gly Asn Lys Arg Pro Gly Asp
530 535 540

Pro Lys His Ser Ser Gln Thr Ser Asn Leu Ala His Lys Thr Tyr Ser
545 550 555 560

Leu Ser Ser Ser Phe Ser Ser Ser Ser Ser Thr Arg Lys Arg Gly Pro
565 570 575

Ser Glu Glu Thr Gly Gly Ala Val Phe Asp His Pro Ala Lys Ile Ala
580 585 590

Lys Ser Thr Lys Ser Ser Ser Leu Asn Phe Ser Phe Pro Ser Leu Pro
595 600 605

Thr Met Gly Gln Met Pro Gly His Ser Ser Asp Thr Ser Gly Leu Ser
610 615 620

Phe Ser Gln Pro Ser Cys Lys Thr Arg Val Pro His Ser Lys Leu Asp
625 630 635 640

Lys Gly Pro Thr Gly Ala Asn Gly His Asn Thr Thr Gln Thr Ile Asp
645 650 655

Tyr Gln Asp Thr Val Asn Met Leu His Ser Leu Leu Ser Ala Gln Gly
660 665 670

Val Gln Pro Thr Gln Pro Thr Ala Phe Glu Phe Val Arg Pro Tyr Ser
675 680 685

Asp Tyr Leu Asn Pro Arg Ser Gly Gly Ile Ser Ser Arg Ser Gly Asn
690 695 700

Thr Asp Lys Pro Arg Pro Pro Pro Leu Pro Ser Glu Pro Pro Pro Pro
705 710 715 720

Leu Pro Pro Leu Pro Lys
725

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TTCCACCAA TGCTTTCC

18

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CCATCAGTTG ATACAGGGAT CT

22

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GGAATTCAGA AGGTTGTAAG ATGC

24

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ACACACAGAT GTGGTGAAAT GTACCCA

27

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GCATCTTACA ACCTTCTG	4200.000200	18
(2) INFORMATION FOR SEQ ID NO:56:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 28 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:		
GGAATTCATG GAAAGCATTG GTGGGAAT		28
(2) INFORMATION FOR SEQ ID NO:57:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 22 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:		
CCTCCACTAC TGGTTTGCCT GG		22
(2) INFORMATION FOR SEQ ID NO:58:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 30 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:		
GGACTAGTAT AAATATGGCG TCGGGCCGTG		30
(2) INFORMATION FOR SEQ ID NO:59:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 27 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:		
GGAGATCTTA CATGTTCAAT CCTTGGG		27
(2) INFORMATION FOR SEQ ID NO:60:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 29 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GGAGACAAGT ATGTGCTACC TTGATGACA

29

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GGAATTCGGG CTGCTCCTCC ACTTTAG

27

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GGAATTCGCT GCTGGAGCCA CAGAA

25

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GTGTCCTGA AAGAATACCG

20

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GGAATTCAGG TGGAGATAAA GCTGC

25

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GCTCTAGATA AATATGGAGG GAGAGAGGAA

30

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GGAATTCTTA CTTAGGAAGG GGTGGAAGTG

30

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GGAATTCTTA CTTAGGAAGG GGTGGAAGTG GTGGAGGAGG TTAC

44

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Ala Cys Ser Tyr Ser Pro Thr Ser Pro Ser Tyr Ser Pro Thr Ser Pro
1 5 10 15

Ser Tyr Ser Pro Thr Ser Pro Ser Lys Lys
20 25